



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/766,535

Source:

OIPE

Date Processed by STIC:

2-7-2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

DATE: 02/07/2001

PATENT APPLICATION: US/09/766,535

TIME: 16:04:32

Input Set : A:\0975.1005-010SEQLIST.txt

Output Set: N:\CRF3\02072001\I766535.raw

4 <110> APPLICANT: Junming Le
 5 Jan Vilcek
 6 Peter Daddona
 7 John Ghrayeb
 8 David M. Knight
 9 Scott Siegel
 11 <120> TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
 12 Human Tumor Necrosis Factor
 15 <130> FILE REFERENCE: 0975.1005-010
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/766,535
 C--> 17 <141> CURRENT FILING DATE: 2001-01-18
 17 <150> PRIOR APPLICATION NUMBER: U.S. 09/133,119
 18 <151> PRIOR FILING DATE: 1998-08-12
 20 <150> PRIOR APPLICATION NUMBER: U.S. 08/570,674
 21 <151> PRIOR FILING DATE: 1995-12-11
 23 <150> PRIOR APPLICATION NUMBER: U.S. 08/324,799
 24 <151> PRIOR FILING DATE: 1994-10-18
 26 <150> PRIOR APPLICATION NUMBER: U.S. 08/192,102
 27 <151> PRIOR FILING DATE: 1994-02-04
 29 <150> PRIOR APPLICATION NUMBER: U.S. 08/192,861
 30 <151> PRIOR FILING DATE: 1994-02-04
 32 <150> PRIOR APPLICATION NUMBER: U.S. 08/192,093
 33 <151> PRIOR FILING DATE: 1994-02-04
 35 <150> PRIOR APPLICATION NUMBER: U.S. 08/010,406
 36 <151> PRIOR FILING DATE: 1993-01-29
 38 <150> PRIOR APPLICATION NUMBER: U.S. 08/013,413
 39 <151> PRIOR FILING DATE: 1993-02-02
 41 <150> PRIOR APPLICATION NUMBER: U.S. 07/943,852
 42 <151> PRIOR FILING DATE: 1992-09-11
 44 <150> PRIOR APPLICATION NUMBER: U.S. 07/853,606
 45 <151> PRIOR FILING DATE: 1992-03-18
 47 <150> PRIOR APPLICATION NUMBER: U.S. 07/670,827
 48 <151> PRIOR FILING DATE: 1991-03-18
 50 <160> NUMBER OF SEQ ID NOS: 19
 52 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 54 <210> SEQ ID NO: 1
 55 <211> LENGTH: 157
 56 <212> TYPE: PRT
 57 <213> ORGANISM: Peptide
 59 <400> SEQUENCE: 1
 60 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
 61 1 5 10 15
 62 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
 63 20 25 30
 64 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
 65 35 40 45
 66 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe

must be 1 of the following:
 1) scientific name "Genus Species"
 2) Artificial Sequence
 3) Unknown

See item 12 on
 ERROR summary sheet

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Input Set : A:\0975.1005-010SEQLIST.txt

Output Set: N:\CRF3\02072001\I766535.raw

67 50 55 60
 68 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Thr His Thr Ile
 69 65 70 75 80
 70 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
 71 85 90 95
 72 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
 73 100 105 110
 74 Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
 75 115 120 125
 76 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
 77 130 135 140
 78 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
 79 145 150 155
 82 <210> SEQ ID NO: 2
 83 <211> LENGTH: 321
 84 <212> TYPE: DNA
 85 <213> ORGANISM: cdna *see page 1 start range at 1*
 87 <220> FEATURE:
 88 <221> NAME/KEY: CDS
 W--> 89 <222> LOCATION: (0)..(321)
 91 <400> SEQUENCE: 2
 92 gac atc ttg ctg act cag tct cca gcc atc ctg tct gtg agt cca gga 48
 93 Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
 94 1 5 10 15
 96 gaa aga gtc agt ttc tcc tgc agg gcc agt cag ttc gtt ggc tca agc 96
 97 Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
 98 20 25 30
 100 atc cac tgg tat cag caa aga aca aat ggt tct cca agg ctt ctc ata 144
 101 Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
 102 35 40 45
 104 aag tat gct tct gag tct atg tct ggg atc cct tcc agg ttt agt ggc 192
 105 Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
 106 50 55 60
 108 agt gga tca ggg aca gat ttt act ctt agc atc aac act gtg gag tct 240
 109 Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
 110 65 70 75 80
 112 gaa gat att gca gat tat tac tgt caa caa agt cat agc tgg cca ttc 288
 113 Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
 114 85 90 95
 116 acg ttc ggc tgc ggg aca aat ttg gaa gta aaa 321
 117 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
 118 100 105
 121 <210> SEQ ID NO: 3
 122 <211> LENGTH: 107
 123 <212> TYPE: PRT
 124 <213> ORGANISM: Protein
 126 <400> SEQUENCE: 3
 127 Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
 128 1 5 10 15

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Input Set : A:\0975.1005-010SEQLIST.txt

Output Set: N:\CRF3\02072001\I766535.raw

129 Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
 130 20 25 30
 131 Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
 132 35 40 45
 133 Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
 134 50 55 60
 135 Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
 136 65 70 75 80
 137 Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
 138 85 90 95
 139 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
 140 100 105
 143 <210> SEQ ID NO: 4
 144 <211> LENGTH: 357
 145 <212> TYPE: DNA
 146 <213> ORGANISM: cDNA
 148 <220> FEATURE:
 149 <221> NAME/KEY: CDS
 W--> 150 <222> LOCATION: (9)..
 152 <400> SEQUENCE: 4
 153 gaa gtg aag ctt gag gag tct gga gga ggc ttg gtg caa cct gga gga 48
 154 Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 155 1 5 10 15
 157 tcc atg aaa ctc tcc tgt gtt gcc tct gga ttc att ttc agt aac cac 96
 158 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
 159 20 25 30
 161 tgg atg aac tgg gtc cgc cag tct cca gag aag ggg ctt gag tgg gtt 144
 162 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
 163 35 40 45
 165 gct gaa att aga tca aaa tct att aat tct gca aca cat tat gcg gag 192
 166 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
 167 50 55 60
 169 tct gtg aaa ggg agg ttc acc atc tca aga gat gat tcc aaa agt gct 240
 170 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
 171 65 70 75 80
 173 gtc tac ctg caa atg acc gac tta aga act gaa gac act ggc gtt tat 288
 174 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
 175 85 90 95
 177 tac tgt tcc agg aat tac tac ggt agt acc tac gac tac tgg ggc caa 336
 178 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
 179 100 105 110
 181 ggc acc act ctc aca gtc tcc 357
 182 Gly Thr Thr Leu Thr Val Ser
 183 115
 186 <210> SEQ ID NO: 5
 187 <211> LENGTH: 119
 188 <212> TYPE: PRT
 189 <213> ORGANISM: Protein
 191 <400> SEQUENCE: 5

— start range at 1

see page 1

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/766,535

DATE: 02/07/2001

TIME: 16:04:32

Input Set : A:\0975.1005-010SEQLIST.txt

Output Set: N:\CRF3\02072001\I766535.raw

```

192 Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
193 1 5 10 15
194 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
195 20 25 30
196 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
197 35 40 45
198 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
199 50 55 60
200 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Ser Lys Ser Ala
201 65 70 75 80
202 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
203 85 90 95
204 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
205 100 105 110
206 Gly Thr Thr Leu Thr Val Ser
207 115

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210 <210> SEQ ID NO: 6

211 <211> LENGTH: 8

212 <212> TYPE: PRT

213 <213> ORGANISM: Protein

215 <400> SEQUENCE: 6

216 Gly Thr Leu Val Thr Val Ser Ser

217 1 5

220 <210> SEQ ID NO: 7

221 <211> LENGTH: 7

222 <212> TYPE: PRT

223 <213> ORGANISM: Protein

225 <400> SEQUENCE: 7

226 Gly Thr Lys Leu Glu Ile Lys

227 1 5

230 <210> SEQ ID NO: 8

231 <211> LENGTH: 20

232 <212> TYPE: DNA

233 <213> ORGANISM: cDNA

235 <400> SEQUENCE: 8

236 cctggatacc tgtgaaaaga

238 <210> SEQ ID NO: 9

239 <211> LENGTH: 27

240 <212> TYPE: DNA

241 <213> ORGANISM: cDNA

243 <400> SEQUENCE: 9

244 cctggtacct tagtcaccgt ctctca

246 <210> SEQ ID NO: 10

247 <211> LENGTH: 27

248 <212> TYPE: DNA

249 <213> ORGANISM: cDNA

251 <400> SEQUENCE: 10

252 aatagatatc tccttcaaca cctgcaa

254 <210> SEQ ID NO: 11

See page 1

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27

27

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/766,535

DATE: 02/07/2001

TIME: 16:04:32

Input Set : A:\0975.1005-010SEQLIST.txt

Output Set: N:\CRF3\02072001\I766535.raw

255 <211> LENGTH: 21
 256 <212> TYPE: DNA
 257 <213> ORGANISM: cDNA
 259 <400> SEQUENCE: 11
 260 atcgggacaa agttggaaat a 21
 262 <210> SEQ ID NO: 12
 263 <211> LENGTH: 16
 264 <212> TYPE: DNA
 265 <213> ORGANISM: cDNA
 267 <400> SEQUENCE: 12
 268 ggcgggtctgg taccgg 16
 270 <210> SEQ ID NO: 13
 271 <211> LENGTH: 19
 272 <212> TYPE: DNA
 273 <213> ORGANISM: cDNA
 275 <400> SEQUENCE: 13
 276 gtcaacaaca tagtcatca 19
 278 <210> SEQ ID NO: 14
 279 <211> LENGTH: 23
 280 <212> TYPE: DNA
 281 <213> ORGANISM: cDNA
 283 <400> SEQUENCE: 14
 284 cacaggtgtg tccccaggga aaa 23
 286 <210> SEQ ID NO: 15
 287 <211> LENGTH: 18
 288 <212> TYPE: DNA
 289 <213> ORGANISM: cDNA
 291 <400> SEQUENCE: 15
 292 aatctgggggt aggcacaa 18
 294 <210> SEQ ID NO: 16
 295 <211> LENGTH: 17
 296 <212> TYPE: DNA
 297 <213> ORGANISM: cDNA
 299 <400> SEQUENCE: 16
 300 agtggtgtgtc cccaagg 17
 302 <210> SEQ ID NO: 17
 303 <211> LENGTH: 24
 304 <212> TYPE: DNA
 305 <213> ORGANISM: cDNA
 307 <400> SEQUENCE: 17
 308 cacagctgcc cgcccagggtg gcat 24
 310 <210> SEQ ID NO: 18
 311 <211> LENGTH: 17
 312 <212> TYPE: DNA
 313 <213> ORGANISM: cDNA
 315 <400> SEQUENCE: 18
 316 gtcgccagtg ctccctt 17
 318 <210> SEQ ID NO: 19
 319 <211> LENGTH: 20

see page 1

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/766,535

DATE: 02/07/2001

TIME: 16:04:33

Input Set : A:\0975.1005-010SEQLIST.txt

Output Set: N:\CRF3\02072001\I766535.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:89 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:2, CDS LOCATION: (0)...(321)

L:150 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:4, CDS LOCATION: (0)...(357)

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/766,535

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) AI are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.
AKS-Biotechnology Systems Branch- 5/15/99